



1/19

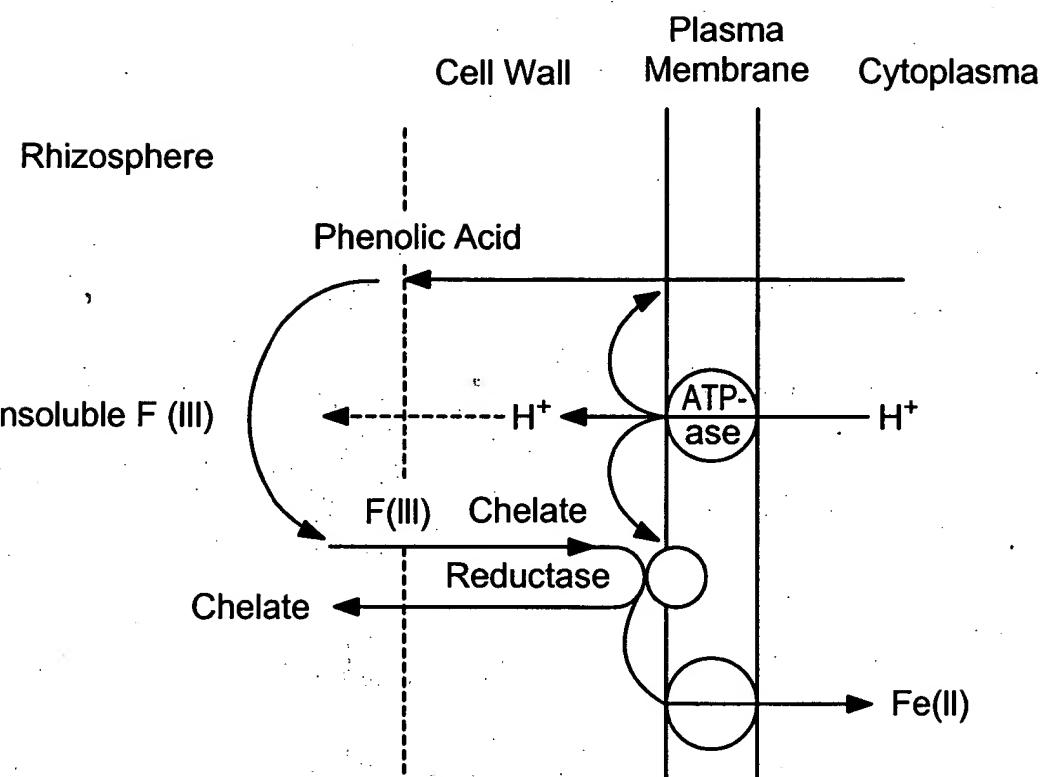
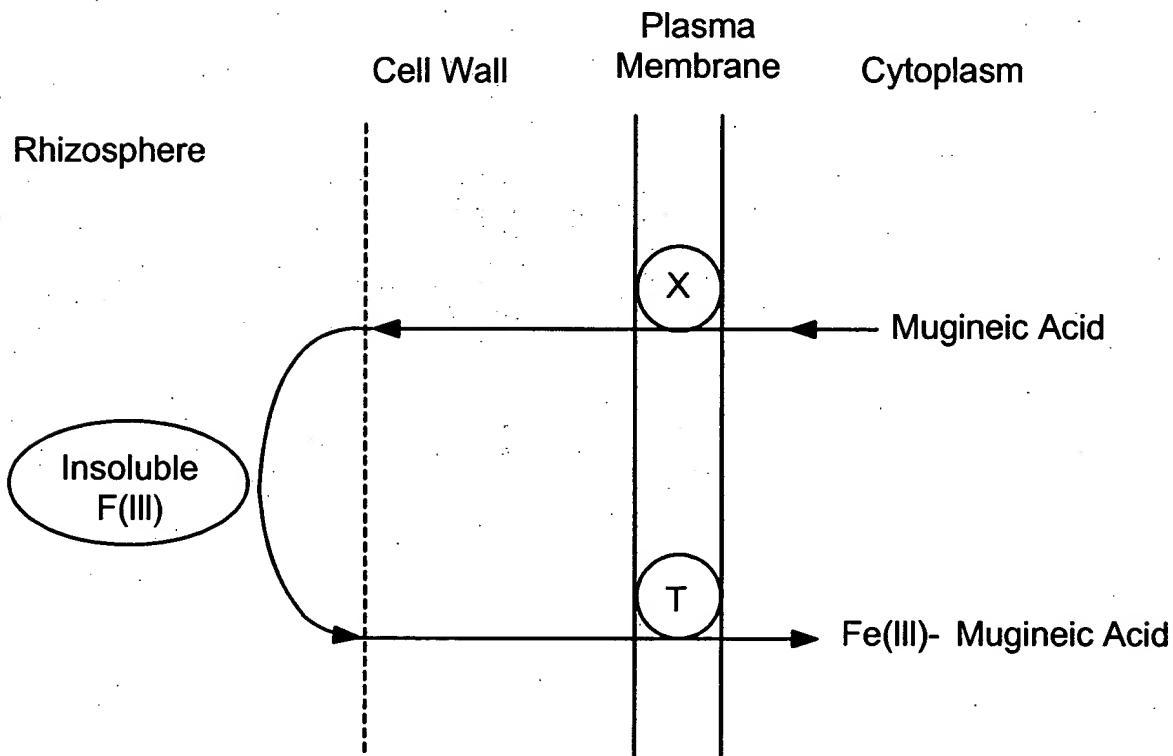


FIG. 1



Two Kinds of Fe-Uptake Mechanisms in Higher Plants

FIG. 2



Seq 37



putative poly(A)
poly(A) signal site
541 TCCGT[AAAAAA]TCACTTATT[ATCCTTCTGTTACAAAGATTATAATGAACTTTTATTATGGAAAGCGTCTACCATTAAATT 630
181 S V K K S L I Y P S V Y K D Y N E R T F Y L W K R L P F N F 210

2/19

putative poly(A)
poly(A) signal site
531 ACAACTCGAGGCAAGGGTCTCGTCGTATTAA[TTTTGTTATTATCTCAGTTGGTCATAATTTAAACTTCCACAC 720
211 T T R G K G L V V L I F V I L T I L S L S F G H N I K L P H 240

FIG. 3



1	ATGGTTAGAACCGTGTATTCTGGTTATTTATCTTTTTGCTACGGTCAATCG	60
61	AGTGCTAGACTTATTAGCACTTCATGTATTCAGCTGGCTGGGTCAGTGACAGCA	120
121	TCTAGTAAATCTAAAAGTGTACTGTAAAACATCAATTGGCTGGGTCAGTGACAGCA	180
181	TGTGCCTATGAGAATTCCAATCTAACAAAACACTAGACAGCGCTTAATGAAGTTAGCA	240
241	TCCCCAATGTTCAAGCATCAAAGTTATCTTACAGGACATGAAGAATTATTTAAAT	300
301	GCGTCAAATTATTGAGAGCACCTGAGAAAAGTGATAAAAAACCGTGGTAGTCAACCG	360
361	CTCATGGCGAACGAGACAGCGTATCATTATTATGAGGAAAATTATGGTATCCATCTT	420
421	AACCTAATGCGCTCTCAATGGTGGGGTGGGTGTGGTCTTGTGGGTGGGTGGTT	480
481	ACTGCAGCCACTATCTGAAACATTCTGAAAAGGTGTGTTGGTAAGAACATCATGGCAAAC	540
541	TCCGTCAAAAATCACTTATTTATCCTCTGTTACAAAGATTATAATGAACGAACCTTT	600
601	TATTTATGGAAGCGTCTACCATTAACTTACAACCTCGAGGCAAGGGTCTCGTGTATTA	660
661	ATTTTGTATTTGACTATATTATCTCTAGTTGGTCATAATATTAAACTCCACAC	720
721	CCATATGATAGGCCAGATGGAGAAGAAGTATGGCCTTGTGAGTCGTAGAGCAGACTTG	780
781	ATGGCCATTGCACTTTCCCAGTAGTCTATCTATTGGAATAAGAAATAATCCCTTCATC	840
841	CCTATAACAGGGCTTCCCTTCTACATTAACTTATCATAAAATGGTCTGCCTACGTT	900
901	TGTTTCATGTTGGCGTTGTACACTCAATTGTCATGACCGCCTCGGGAGTGAAAAGAGGT	960
961	GTGTTCAAAGTCTGGTTAGGAAATTAACTTAGTGGGTATAGTGGCAACGATATTA	1020
1021	ATGTCTATTATTATTTCCAAAGTAAAAAGTATTAGAAATAGAGGGTATGAGATATTC	1080
1081	CTTCTTATTCAAAAGCGATGAATATTATGTTATTGCCATGTACTACCATTGTCAC	1140
1141	ACCGTGGCTGGATGGGTGGATTGGTCAATGGCTGGTATTATGCTTGTAGATTC	1200
1201	TGCAGGATTGTTAGAATAATCATGAATGGTGGCTGAAAAGTCTACTTGTAGTACCACT	1260
1261	GATGATTCTAATGTTATTAACATTCACTGAGTAAAAACCAAAGTTTCAAGTACCAAGTA	1320
1321	GGAGCTTCGCACATGTATTCTTACACAAAAAGTGCATGGTCTATAGTTCAA	1380
1381	TCACATCCATTACAGTATTATCGGAACGACACCGTGATCCAACAAATCCAGATCAATTG	1440
1441	ACGATGTACGTAAGGCAAATAAAGGTATCAGTGGTTATGAAAGTTCTAAGT	1500
1501	GCTCCAAATCATACTGTTATTGAAATATTCCCTGAAGGCCATATGGTGTAAACGGTT	1560
1561	CCACATATCGCTAACGCTAAAAGAAATCTGGTAGGTGTAGCCGTGGTTGGGTGTTGCG	1620
1621	GCTATTATCCGCACTTGTCGAATGTTACGGTTACCATCTACTGATCAACTCAGCAT	1620
1681	AAATTTCAGTGGATTGTTATGACCTATCCATTGAAATGGTTGAAAATGAATTGCAA	1740
1741	TGGTAAAGGAGAAAAGTGTGAAGTCTCAGTCATATATACTGGTCCAGTGTGAGGAC	1800
1801	ACAAATTCACTGAGAGTACAAAGTTGATGATAAAGAAGAAAGCGAAATCACTGTT	1860
1861	GAATGTCTCAATAAAAGACCTGATTGAAAGAAACTAGTGCCTCGGAAATAACTCTCA	1920
1921	GAACTAGAGAATAATAATTACCTTTATTCCCTGCAGCAACGTTAACGACGAT	1980
1981	TTTAGAAATGCAGTGGTCCAAGGTATAGACTCTCCTGAAGATTGACGTTGAACTAGAA	2040
2041	GAAGAAAGTTTACATGGT	2059

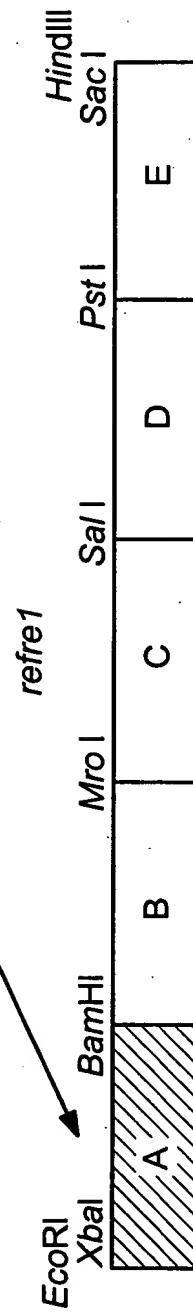
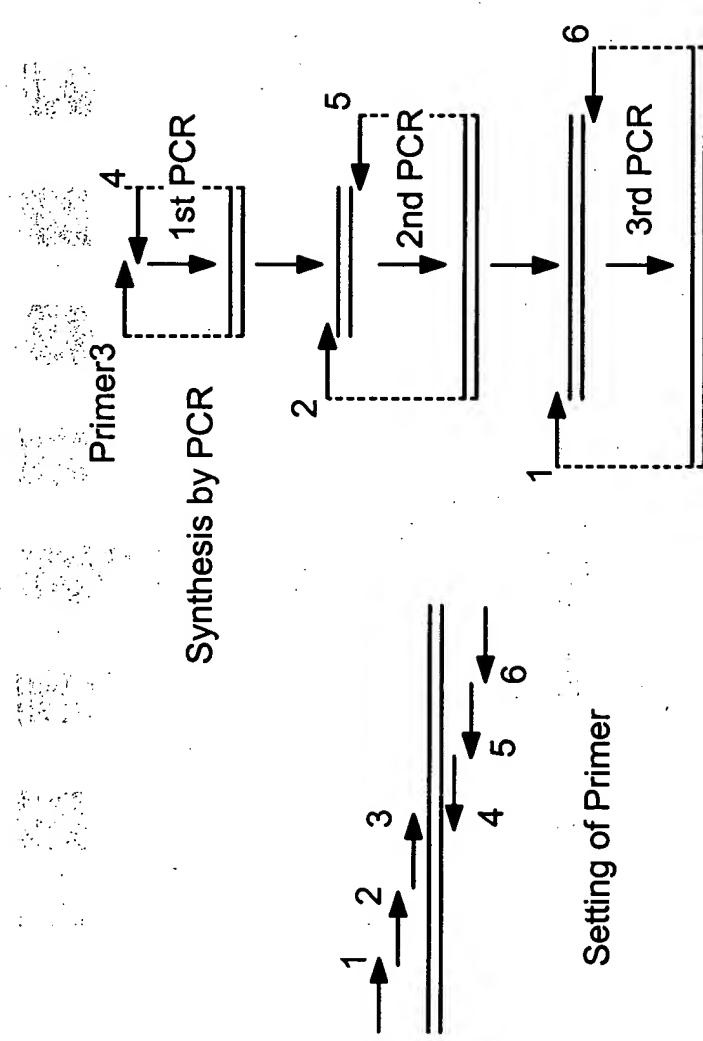


FIG. 5

1,7 429 840 1270 1691 2081,2087

1,7



Sequence Name Base Sequence

5'

A-1	GAATTCTAGACTCCACCATGGTTAGAACAGACTCCTTTCTGCCTCTTCAATCTCTTCAGGTACAGTCCAATCGAGCG	83mer
A-2	GTCCAATCGAGGCTACACTCATCTCCACTCTACAGCTTCTCAGGGTGCACCTGACTGTAACCTGGATGCTCAAGGAAGTCMAA	83mer
A-3	CAAGCAAAGTCAAAGCTTGGCTACTGCAAGAACATCAATTGGCTCGGAAGGCTACACTGCATGGCCTTATGAGAACCTCCAATCT	83mer
A-4	TCCAGTGTGTTAACCTTGACTCTGAGCATGGCTGGCAAGTTTCATCAAGGGAGTCAGAGCTTGTAGATTGGAGTT	83mer
A-5	TGTCTCTTATCGGATTCTCAAGGAGCGGAAGGTAGTTACTGCATTAAGGTAGATGTCTCATGCTCTCAGTGTGTAAGAA	83mer
A-6	GTATGCCATAGTTCTCATAGTAGTGTATAGCTTCAACCGGTCTCATTTGCCATCAACGGTTGTGTAAGAACAAACTGTCTTCTTATCG	83mer

3'

FIG. 6A

FIG. 6B

FIG. 6

5/19

B-1	GGATCCACTTGAATTGATGCCATCTCAATGGTGGCATGGGGCTCGCTCTTCTGGTGGCAAGTCCCTTACGGCCGA	80mer
B-2	CCTTACCGGGCGAACTATCTGAACATTCTAAACGGGTATTGGCAAGAACATTATGGAAATTCTGTTAAGAACGTCTC	80mer
B-3	GTAAAGAAGTCTCTTATCTACCCAAAGGGTTACAAAGACTACAACGGAGAAACTTCTATCTTGGAAACGTTGCCATT	80mer
B-4	AGAGTGAAGAGAATAGTCAAGATGACAAGATAAGAACTACAGACTTGGCTCGAGTTGAAGTGAATGGCAAACGT	80mer
B-5	ATGCCATGATCTCTCCATCTAGGTCTATCGATGTTGCGCAACTTGTATGTTATGTCGAAAGAGACTGAGAAT	80mer
B-6	TCCGGATACCGAAAAGGTACACCAACGGGAAAAGAGGATGCCATCAAGTCAGGCCATGCAATGGCAATGCCATTTGAT	80mer
C-1	TCCGGAAACACCCCTCATCCCATCACCGGATTGAGCTTACACTTTACACAAATGGTCAAGCATACGTCTGC	83mer
C-2	GCATACGTCGCTTCATGTTAGCCGTGTCATTCATCGTTAGCCATGGCTTCAAGGGAGTAAACGGAGGATTCCAGTCT	83mer
C-3	TATCCAGTCTCTGTAAGGAATTCTACTCAGATGGGAATAGTAGCCAAATCTATGTCATCATTTCCAGTCC	83mer
C-4	ATAAACATGATGTTCATGGCTTGTGAATAAGTAAGAAAGATTTCATAACCTCGGTTCTGAAGACCTTCTGGACTGAAAT	83mer
C-5	GAGGATGCCAGCCATGGACCAGATCCAGGCCATCCATCTAGTGTGGCAATGGTAATACATAGCTATGATAAACATGATG	83mer
C-6	GTGACACAAAGTGGGGCTTAAGACCTCCGTTCATGATGATAACGTACAATTGGCAGAACCTGTGCGAAGCAGGGATGCCAGC	83mer

FIG. 6A



6/19

D-1	GTCGACCACAGATGATTCTAACGTTATCAAGATCTGTCAAGAACGCC	82mer
D-2	GGAGCATTGCCTATATGTACTTCTTCAACAAATCAGCCTGGTTCTACAGTTTCAATCTCATCAGCTCTAACAGGGCATT	82mer
D-3	TTCACAGTCCTATCAGAAAGGCCAGATCAACTAACTATGTAACGTCAAAGCTAACAGGGCTTAAGAAGTACTCTCGTAATGCCCTTGT	82mer
D-4	CCTCTAAAGAAAATCTTGCATTCAACGGTATGGTTGGAGCCGTTAGAACTTGTAGCTTGTCAAGTAACTGTTAGCTTGT	82mer
D-5	GGCCCGCAGGTACTCCTACTAGATTGTCTTAAGTTGTCAATGTAAGGACAGTTACGCCATATGGTCCCTTAAGAAAT	82mer
D-6	CTGCAATTGATCAGTGTAGGCAATCTAACGGATTCAAGGAAATGGGTAGATGGCTGACAGGGCCACGGCGAGGGCCAGCTACT	82mer

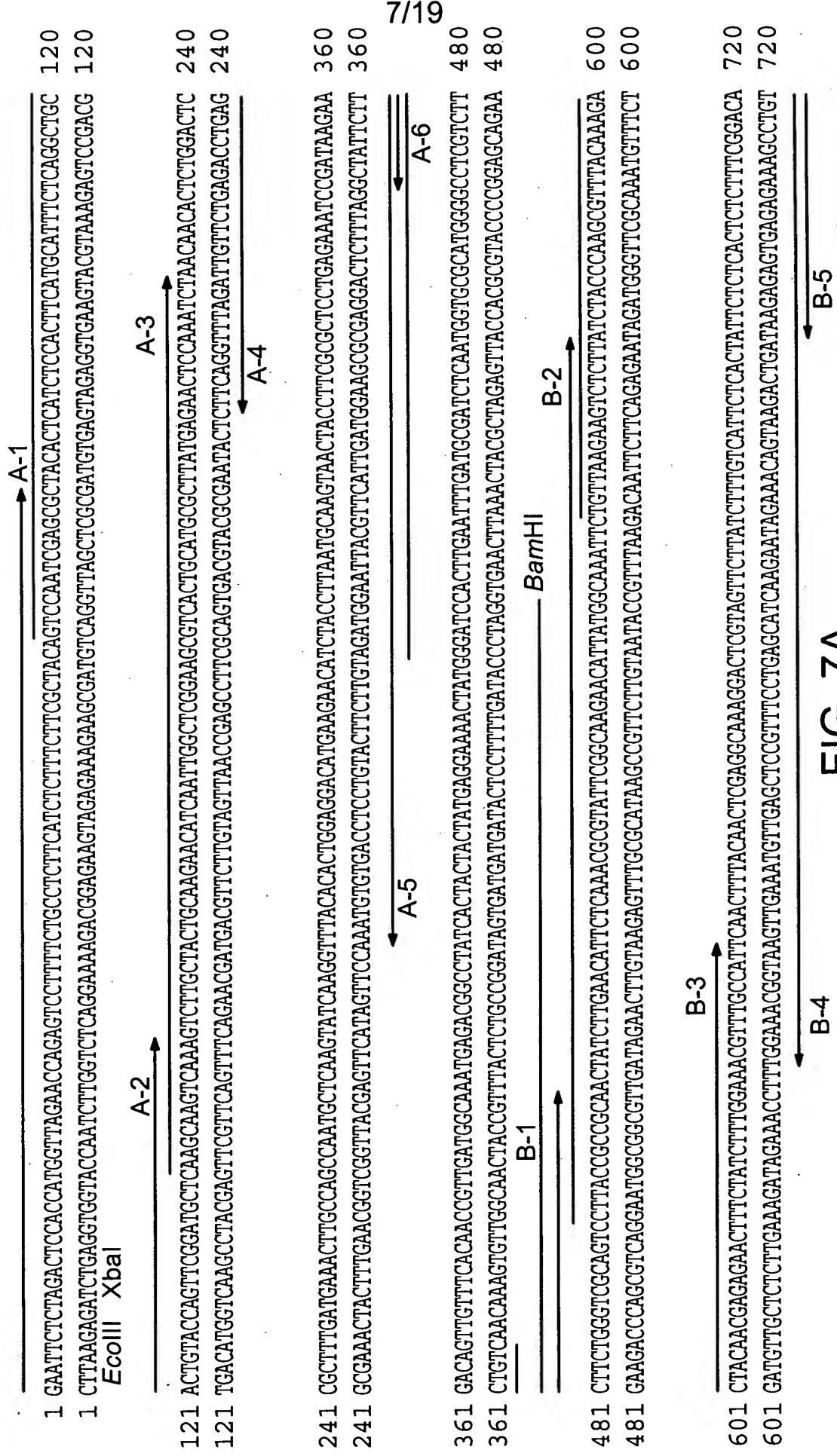
E-1	CTGCAGCACAAAGTTCTACTGGATCGTCAACGCCCTTAACTGTCACCTTAAGTCAAGTGGCTAACAAACGAGCTAACATGGCTAA	77mer
E-2	ACAATGGCTTAAGGAAAATCTTGTGAAGTCTGTCACTACACTGGTCACTGAGGATACAAACTCAGATG	77mer
E-3	CAAACCTCAGATGAGTCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCTAACAAAGGG	77mer
E-4	GTTGATGTTGTTGTTCTCGAGTTCTGATCTCAATTGATCTGACATTGCAAACTTGTCACTAGCTCTGAGGTCTGGCTCTGTAAAG	77mer
E-5	CGATAACCTTGTACAACACTGGCATTCAAGTGTCAATTGAAAGTGTCACTGAGTAAAGTGTAGAATGTTGTTG	77mer
E-6	AAGCTTGAGCTCTTACCAAGTAAACCTCTCCCTCTAGTTGACATCTATCTCAGACTAGAATCGATAACCTTGTAA	77mer

FIG. 6B

FIG. 7B

FIG. 7C

FIG. 7



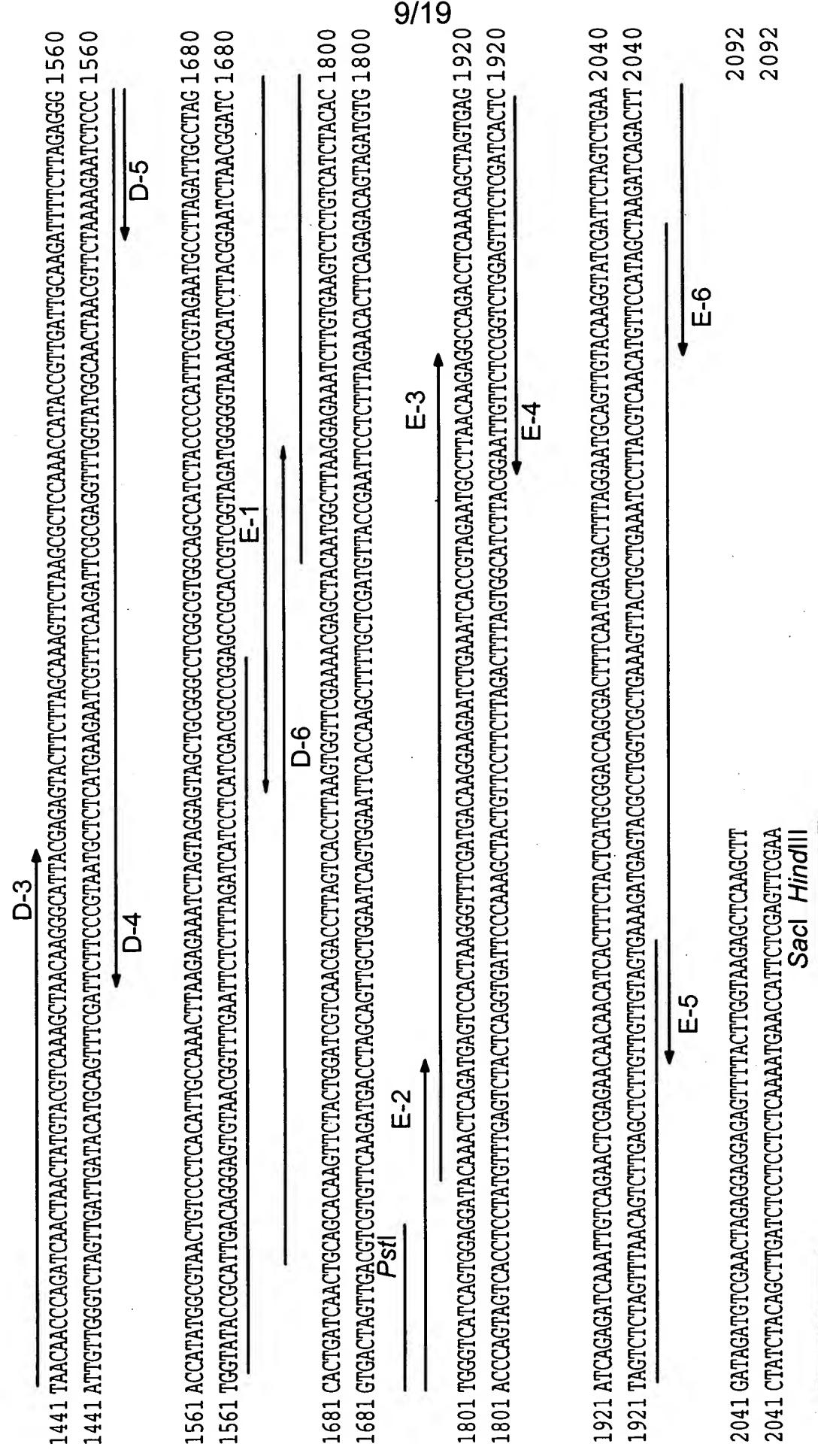


FIG. 7C



10/19

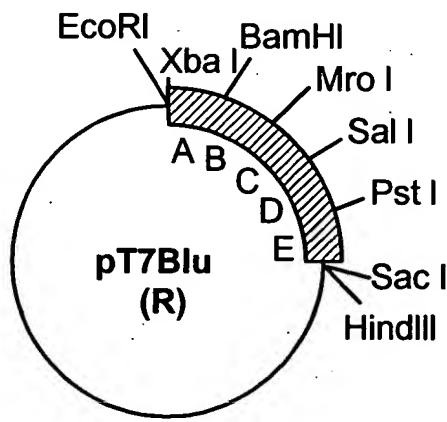
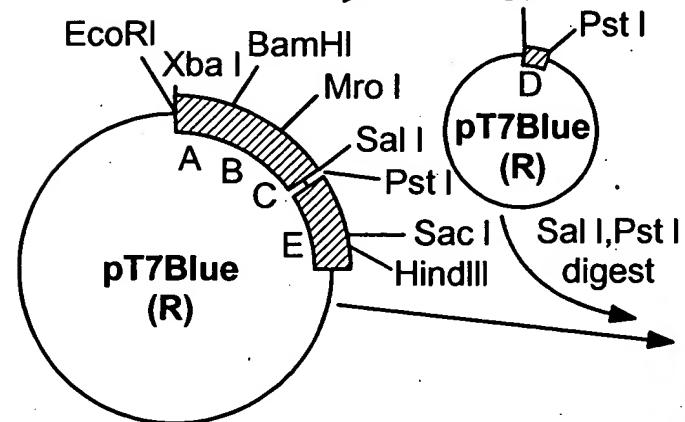
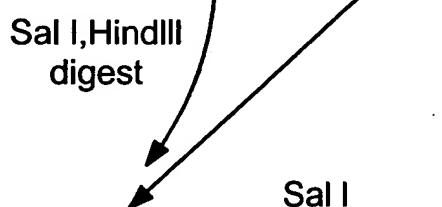
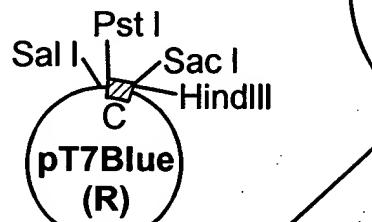
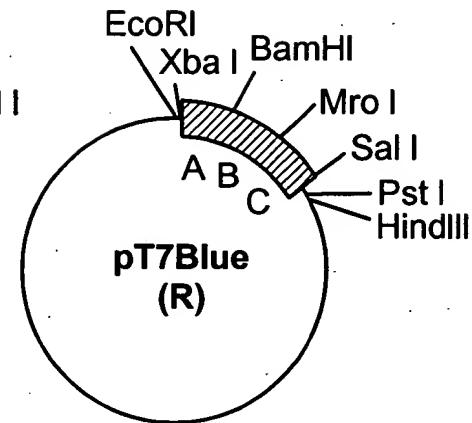
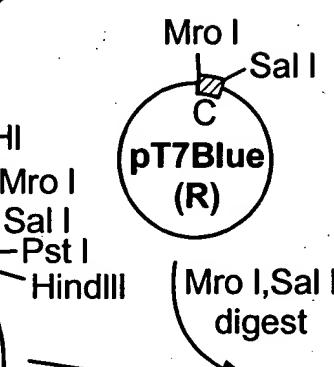
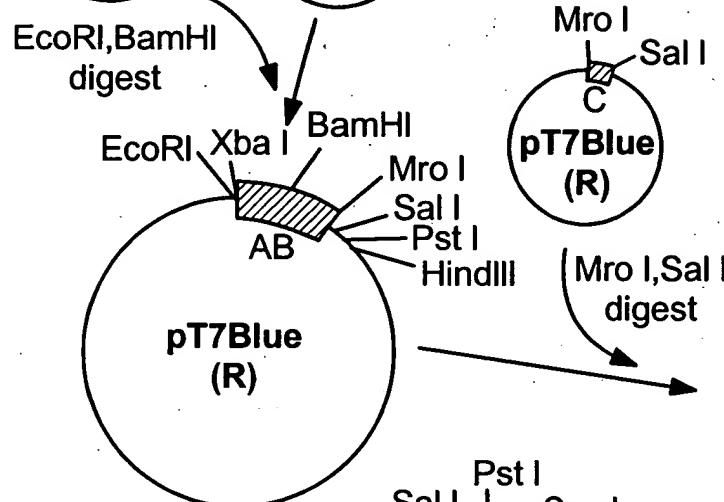
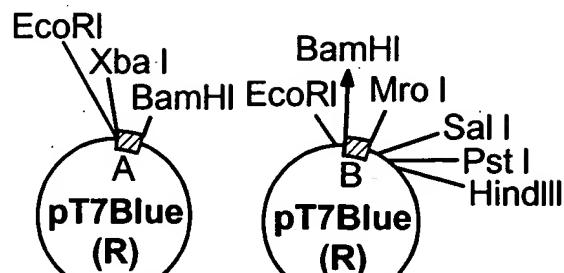


FIG. 9A

FIG. 9B

FIG. 9C

FIG. 9

FIG. 8



1

gaattctctagactccacc 19

20 ATGGTTAGAACCGAGTCCTTCTGCCCTCTCATCTCGCTACAGTCCAATCGAGGCTACACTCATCTCCACTTCATGCATT 109
 1 M V R T R V L F C L F I S F F A T V Q S S A T L I S T S C I 30

110 TCTCAGGCTGCACTGACTGTACCGATTGGATGCTCAAGCAAGTCAAAGTCTTGGCTACTGCAAGAACATCAATTGGCTCGGAAGGGTCACTGGCA 109
 31 S Q A A L Y Q F G C S S K S C Y C K N I N W L G S V T A 60

200 TCGGCTTATGAGAACATCCAATCTAACCAAGACTCTGGACTCCGGTTGATGAAACTTGCAGCCAATGCTCAAGTATCAAGGTTACACCA 289
 61 C A Y E N S K S N K T L D S A L M K L A S Q C S S I K Y Y T 90

11/19

290 CTGGAGGACATGAGAACATCTAACCTTAATGCAAGTAACCTACCTACCTGGAAACTATGGGATCCACTTGCCTGAGAAATCCGATAAGAACAGACTGTTTCAACAAACCG 379
 91 L E D M K N I Y L N A S N Y L R A P E K S D K K T V V S Q P 120

380 TTGATGGCAAATGAGAACGACGGCCTATCACTACTATGAGGAAACTATGGGATCCACTTGCCTGAGAAATCCGATCTCAATGGCATGG 469
 121 L M A N E T A Y H Y Y Y E N Y G I H L N L M R S Q M C A W 150

470 GGCCTCGCTTCTGGGTCTGGCAGTCCTTACCGCCGCAACTATCTTGACACATTCTCAACCCGTTACGGCAAGAACATTATGGCAAAT 559
 151 G L V F F W V A V L T A A T I L N I L K R V F G K N I M A N 180

560 TCTGTTAAGAACGTCTCTTACCCCAAGCGTTTACAAAGACTAACAGAGAGAACCTTCTATCTTGGAAACGTTGCCATTCAACTTT 649
 181 S V K K S L I Y P S V Y K O Y N E R T F Y L N K R L P F N F 210

FIG. 9A

650 ACAACTGGCAAGGACTCGTAGTTCTTGTCACTATTCTGACTTCTCTCACTCTTGGACATAACATCAAGTTGCCACAT
211 T T R G K L V V L I F V I L T I L S F G H N I K L P H 210

740 CCTTACCGATAGACCTAGATGGAGAAGATCAATGGCATTCTGCTCACGCCGTGCTGACTTGATGGCAATCGCTCTTCCCCGTGGTGTAC
241 P Y D R P R W R S M A F V S R R A D L M A I A L F P V V Y 270

830 CTTTCGGTATCCGGAACAAACCCCTTCATCCCAATCACCGGATTGAGCTTACTTCAACTTTACCAAAATGGTCAGCATACGTC
271 L F G I R N N P F I P I T G L S F S T F N F Y H K W S A Y V 300

920 TGCTTCATGTTAGCCGTCCATTCAATCGTTATGACCCGCTTCAGGAGTTAACCGAGGATTCTCAGTCTCTGTAAAGGAATCTAC 1009
301 C F M L A V V H S I V M T A S G V K R G V F G S L V R K F Y 330

1010 TTCAGATGGGAATAGTAGGCCACAAATTCTTATGTCCATCATCATCATTTCAGTCCAGGAAGGGTCTTCAGGAACCCGAGGTATGAAATCTTC 1099
331 F R W G I V A T I L M S I I F Q S E K V F R N R G Y E I F 360 12/19

1100 TACTTATTCAAAAGCCATGAACATCATGTTTATCATAGCTTATGTTATCATGCCACACTAGGATGGATGGCTGGATCTGGTCC 1189
361 L L I H K A M N I M F I I A M Y Y H C H T L G W M G W I W S 390

1190 ATGGCTGGCATCCTCTGCTTCGACAGGTTCTGCCGAATTGTACGTATCATGAAACGGAGGTCTTAAGACGCCACTTGTGCGACCA 1279
391 M A G I L C F D R F C R I V R I I M N G G L K T A T L S T T 420.

1280 GATGATTCTAACGTTATCAAGATCTCTGTCAGGCTTAAGTTCTCAAGTGGAGCATTGCTATATGTTCTTCA 1369
421 D D S N V I K I S V K P F K Y Q V G A F A Y M Y F L S 450

1370 CCAAAATCAGCCTGGTTCTACAGTTCAATCTCATCCCTAACAGTCTTCAAGGACAGAGATCCTAACACCCAGATCAACTA 1459
451 P K S A W F Y S F Q S H P F T V L S E R N R D P N N P D Q L 480

FIG. 9B



1460 ACTATGTACGGTAAAGCTAACAGGGCATTACGGAGACTTCTAGCAAAGTCTTAAGGGCTCCAAACCATACCGTTGATTGCAAGATT 1549
 481 T M Y Y K A N K G I T R V L L S K Y L S A P N H T V D C K I 510
 1550 TTCTTAGGGGACCATATGGCGTAACGTCCCTCACATTGCCAAACTTAAGAGAAATCTAGTAGGAGTAGCTGGATCTGGCTGGGGCTGGCA 1639
 571 F L E G P Y G V T V P H I A K L K R N L V G V A A G L G V A 570
 1640 GCCATCTACCCCCATTCTGTTAGAATGCCCTAGATTGCGACTGATCAAACGGCACAAAGTTCTACTGGATCGTCAACGACCTTAGT 1729
 541 A I Y P H F V E C L R L P S T D Q L Q H K F Y W I V N D L S 570
 1730 CACCTTAAGTGGTTCGAAAACGGCTTACAATGGCTTAAGGAGAAATCTTGTGAAGTCTCTGTCATCTACACTGGGTCACTCAGTGGAGGAT 1819
 571 H L K W F E N E L Q W L K E K S C E V S V I Y T G S S V E D 600
 1820 ACAAACTCAGATGAGTCCACTAAGGGTTTCGATGACAAGGAAGAATCTGAAATCACCGTAGAATGCCCTAACAGAGGCCAGACCTCAA 1909
 601 T N S D E S T K G F D K E S E I T V E C L N K R P D L K 630
 1910 GAGCTAGTGGAGATCAGAGATCAAATTGTCAAGAAACTCGAGAACATCACTTCTACTCATGCCGGACCCAGGACTTCAATGACGAC 1999 13/19
 631 E L V R S E I K L S E L E N N I T F Y S C G P A T F N D D 660 19
 2000 TTTAGGAATGCAGTTGTACAAGGTATCGATCTAGTCTGAAGIATAGATGTCGAACTAGAGGGAGAGTTTACTTGGTAA 2089
 661 F R N A V V Q G I D S S L K I D V E L E E S F T W * 687
 2090 ctt

FIG. 9C



14/19

FRE1

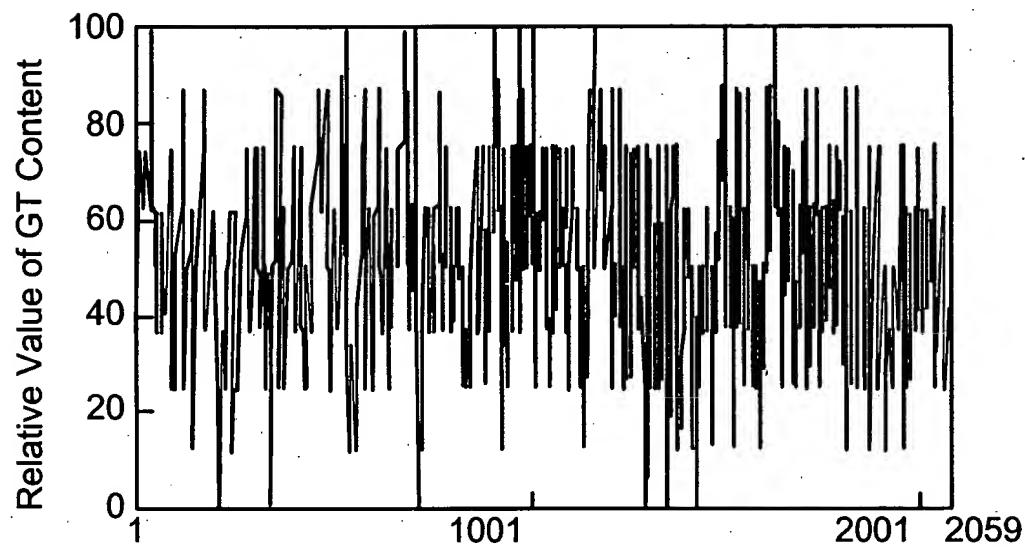


FIG. 10A

refre1

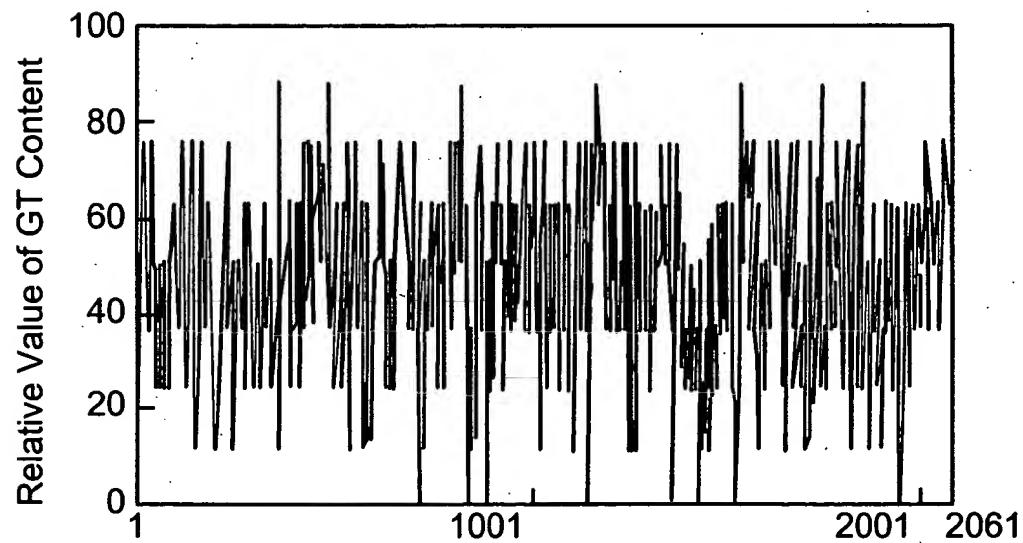


FIG. 10B



15/19

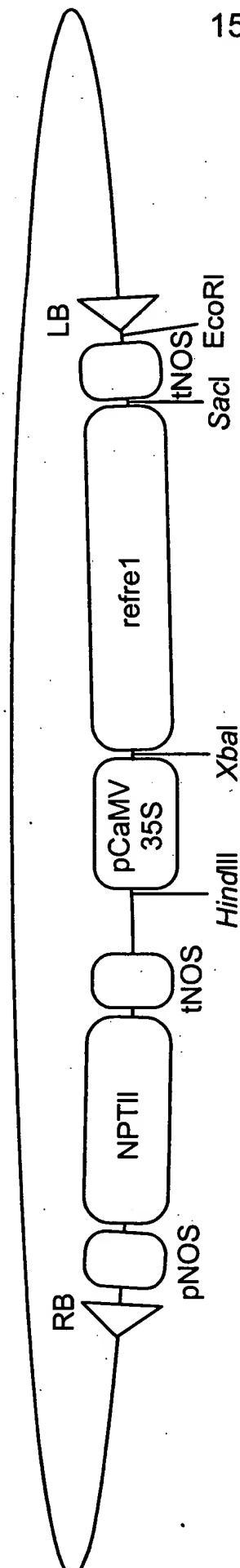


FIG. 11



16/19

BEST AVAILABLE COPY



FIG. 13

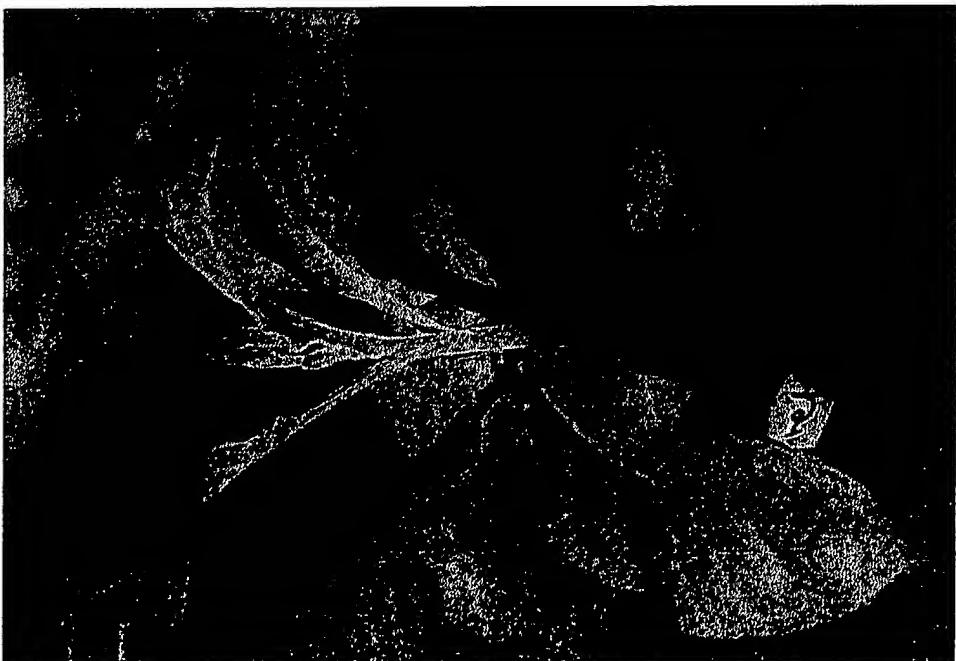


FIG. 12



BEST AVAILABLE COPY

17/19

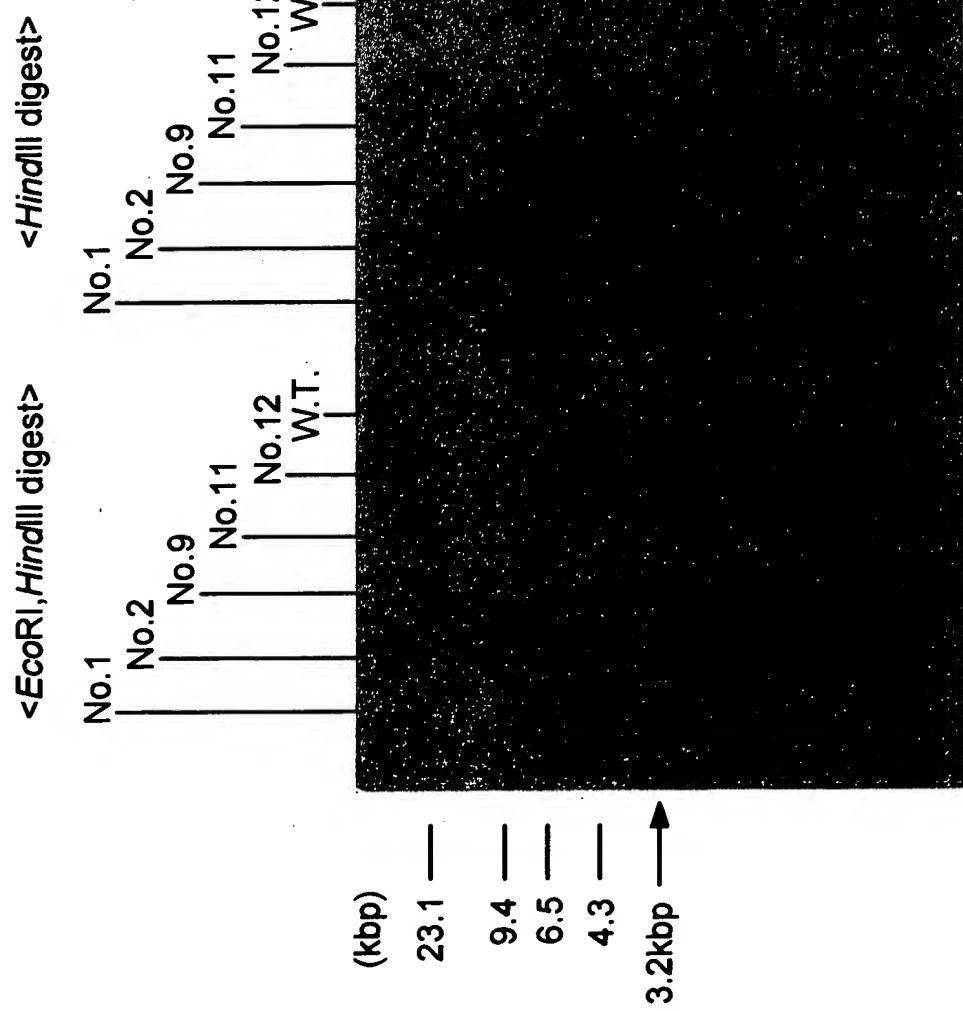
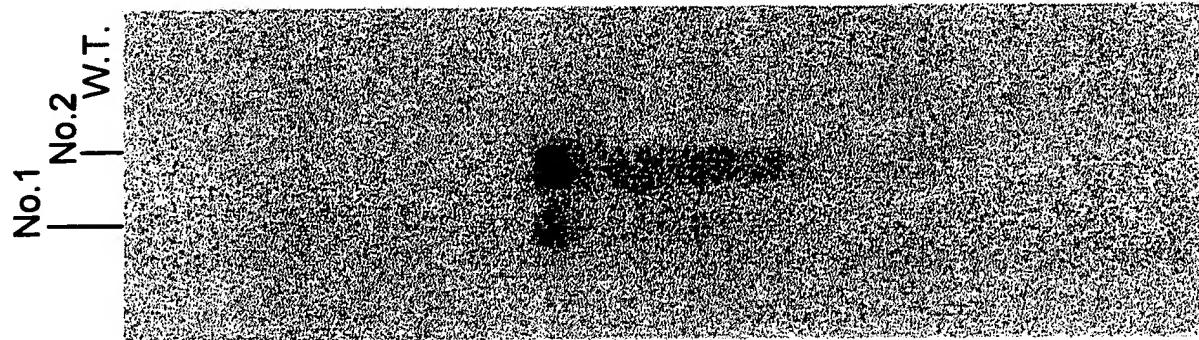


FIG. 15

FIG. 14



BEST AVAILABLE COPY

18/19

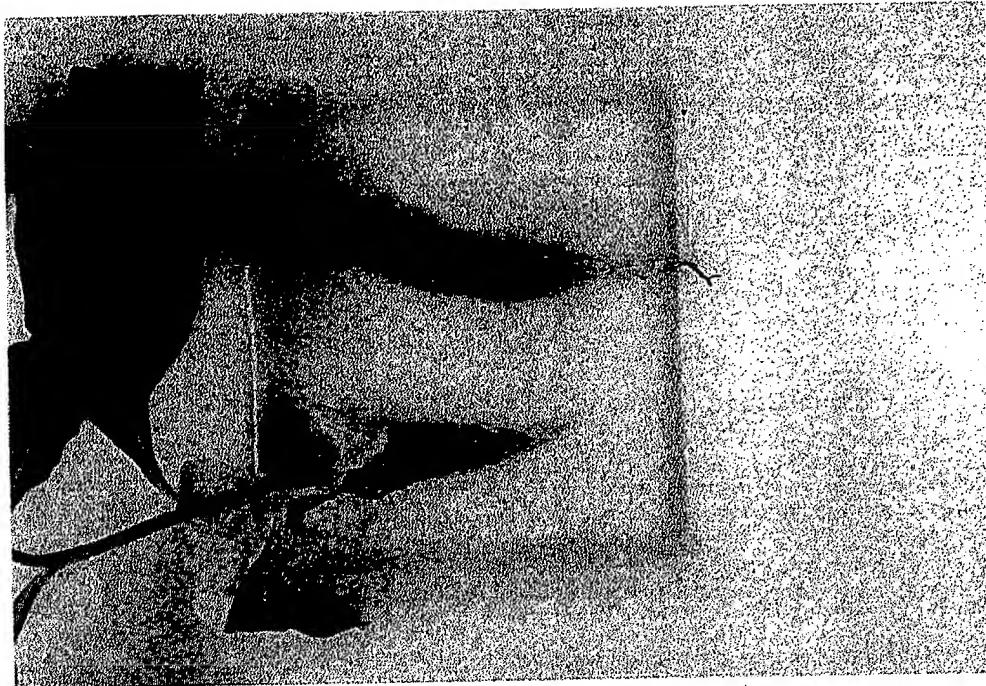


FIG. 17

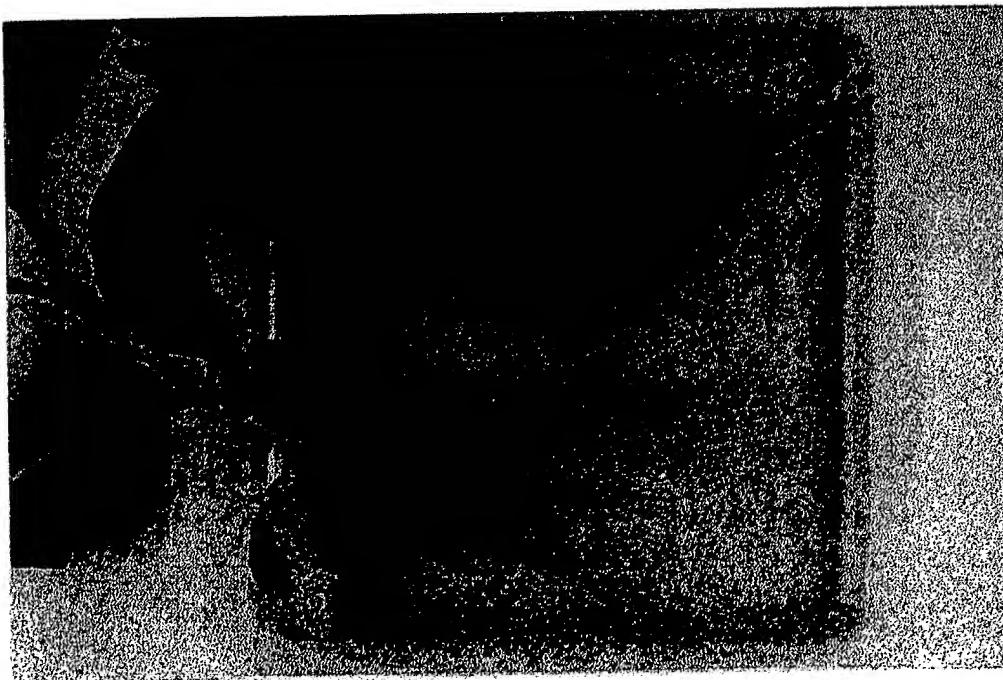


FIG. 16



19/19

BEST AVAILABLE COPY



T₂ Plants

FIG. 18